```
ACGTTGACAC AGGAATGAAG AGTGTATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC      60
ATGTGCTTTT TAAATTGGCC TGCGTGACCC GCCCACTTGG TGTAAAAGAA GAACCGGCCA     120
AAGGGAGGGC CTGAAGGACC TCCACAGGAG TGTGAGCAGC ACTGCTTCAG CAACAAAGCC     180
TCAGGTCCAC ATCTTGGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC         231
                          Met Ala Thr Ser Trp Gly Ala Val Phe
                           1               5

ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG       279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
10                  15                  20                  25

CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT       327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
                30                  35                  40

GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT       375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
            45                  50                  55

GGA ACT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG       423
Gly Thr Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
        60                  65                  70

CTC CCC TTT CTG GAA GGT GAA ATT TTT GAT TCT GTG AAG CCG GGA CTT       471
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu
    75                  80                  85

TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG       519
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu
90                  95                  100                 105

CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG       567
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg
                110                 115                 120

ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG       615
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu
            125                 130                 135

CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT       663
Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn
        140                 145                 150

TCA CCT TTC CTG GTC CCA GAT GGC AGC GTT AGC ATC ATG GAT GGG TCC       711
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser
    155                 160                 165

TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG       759
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln
170                 175                 180                 185

CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT       807
Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly
                190                 195                 200

GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA       855
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu
            205                 210                 215

CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT       903
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr
        220                 225                 230
```

FIG. 1

```
TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA      951
Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala
    235                 240                 245

AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT      999
Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His
250                 255                 260                 265

ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC     1047
Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile
                270                 275                 280

TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG     1095
Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met
            285                 290                 295

GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA     1143
Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys
        300                 305                 310

CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT     1191
Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser
    315                 320                 325

TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG     1239
Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys
330                 335                 340                 345

GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG     1287
Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val
                350                 355                 360

TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG     1335
Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met
            365                 370                 375

GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC     1383
Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala
        380                 385                 390

GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC     1431
Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp
    395                 400                 405

TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT     1479
Trp Leu Gly Leu Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His
410                 415                 420                 425

CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA     1527
His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro
                430                 435                 440

GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT     1575
Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser
            445                 450                 455

GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTTT   1629
Gly Lys Ala Trp Pro Glu Thr Arg
        460                 465
```

FIG. 1 (cont'd.)

```
TAGATGAGTC TTGCTCTTGA GCCTAGTGAT TTGGGCTTCA ATGATTTGCA CATCTAATGT   1689
GAATAGCTCC TAACCACTTG GTGGGTGCAT GGCTGGCACC AGACTGTAAA TCTTTTGGGA   1749
TTCTTTGTAC AGAGTCCTGC AAAGGAAAAA AGAGAAAAGG TTTGGAACTC CATGCTAGAT   1809
TGCGAGTTCA GAGACAGGTC CCTGGGGACC AAAGAACAAT CTCGTTTCAA CCCTTGGATG   1869
CCTCATTGCT TTGAATGGAT TCATTTTTGC TTATAAGCTG ATTTACTGAA ATCCCATAAC   1929
CCATCAATGC TGTTAATTTT TTTCTTCCTA CCCTTATTAC ATTCCCTACC CTAAAAGCCT   1989
GGGGGAAATA CCTGGTTTTG CTTCCCATCT ATAATTGAGA AAGAGGGGGG AAAAGATACT   2049
GTATTAGAAT TTGTGTGATC CTGTGGCACA ATAGATCAAC CAACCCATTT AAAGCTTAAA   2109
AAAAAAAAAA                                                          2119
```

FIG. 1 (cont'd.)

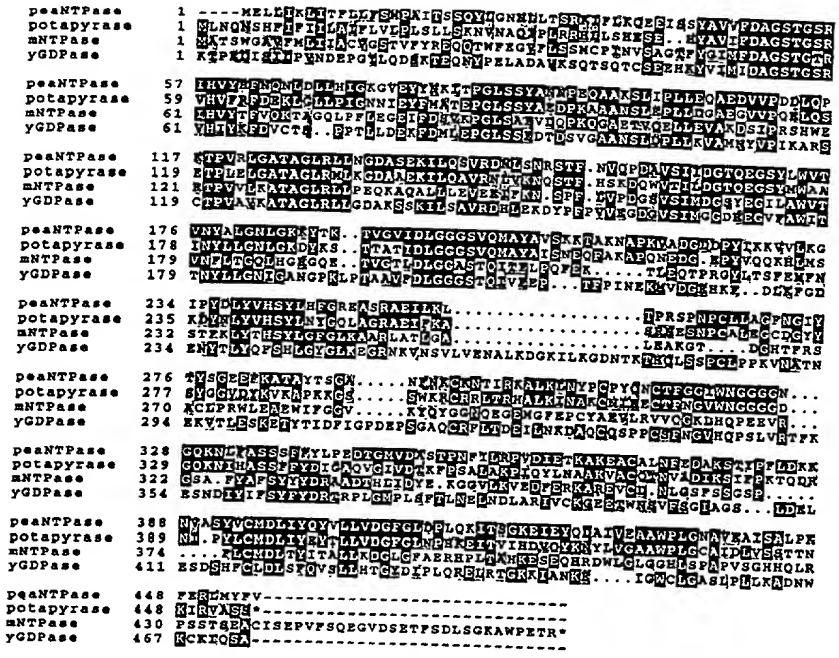
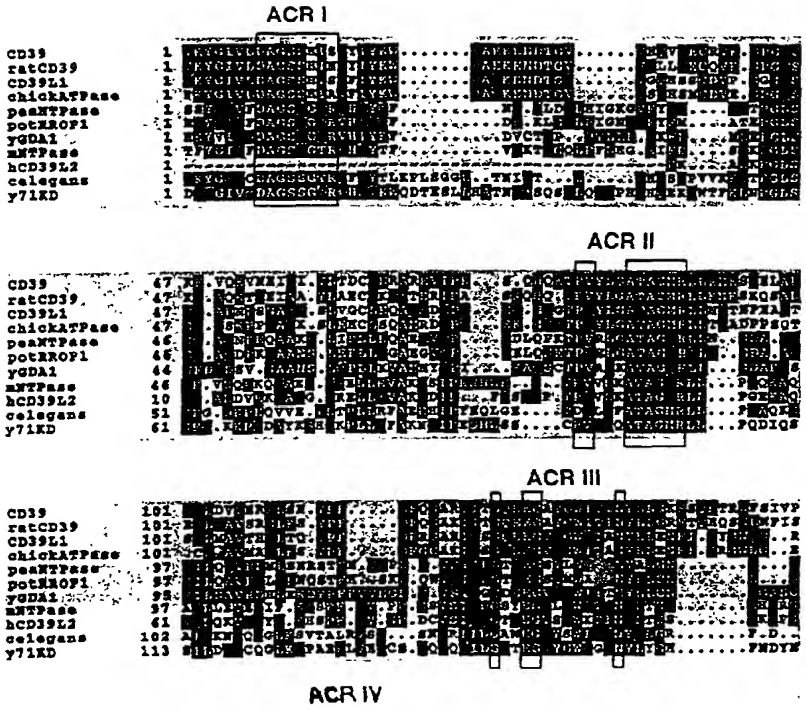


FIG. 2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ACR II
ACR III
ACR IV
CD39
ratCD39
CD39L1
chickATPase
peaNTPase
potNROP1
yGDA1
NTPase
hCD39L2
celegans
y71KD

F16.3

```
GTGGGGTCGT ATCCCGCGGG TGGAGGCCGG GGTGGCGCCG GCCGGGGCGG GGGAGCCCAA     60
AAGACCGGCT GCCGCCTGCT CCCCGGAAAA GGGCACTCGT CTCCGTGGGT GTGGCGGAGC    120
GCGCGGTGCA TGGAATGGGC TATGTGAATG AAAAAAGGTA TCCGTTATGA AACTTCCAGA    180
AAAACGAGCT ACATTTTTCA GCAGCCGCAG CACGGTCCTT GGCAAACAAG G ATG AGA    237
                                                          Met Arg
                                                            1

AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC      285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
          5                  10                  15

CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG      333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
     20                  25                  30

CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC      381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
35                  40                  45                  50

CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT      429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
                55                  60                  65

GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC      477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
            70                  75                  80

ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA      525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu
        85                  90                  95

ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT      573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu
    100                 105                 110

TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA      621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu
115                 120                 125                 130

CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC      669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala
                135                 140                 145

ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA      717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly
            150                 155                 160

GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA      765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala
        165                 170                 175

TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA      813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr
    180                 185                 190

GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC      861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser
195                 200                 205                 210

TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA      909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly
                215                 220                 225
```

FIG. 4

```
GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG      957
Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln
            230                 235                 240

GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC     1005
Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr
        245                 250                 255

TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA     1053
Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala
    260                 265                 270

CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA     1101
Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly
275                 280                 285                 290

AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG     1149
Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp
                295                 300                 305

GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA     1197
Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala
            310                 315                 320

AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC     1245
Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn
        325                 330                 335

AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC     1293
Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe
    340                 345                 350

TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG     1341
Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
355                 360                 365                 370

AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC     1389
Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr
                375                 380                 385

GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC     1437
Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
            390                 395                 400

ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC     1485
Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
        405                 410                 415

AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC     1533
Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
    420                 425                 430

AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA     1581
Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
435                 440                 445                 450

CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG CAGTGTCT  1637
Gln Lys Ser Pro Ala Ser
                455

GTGTGTCTGC ATAAACCCTC CTGTCCTGGA CGTGACTTCA TCCTGAGGAG CCACAGCACA  1697
GGCCGTGCTG GCACTTTCTG CACACTGGCT CTGGGACTTG CAGAAGGCCT GGTGCTGCCC  1757
TGGCATCAGC CTCTTCCAGT CACATCTGGC CAGAGGGCTG TCTGGACCTG GGCCCTGCTC  1817
```

FIG. 4 (contd.)

```
AATGCCACCT GTCTGCCTGG GCTCCAAGTG GGCAGGACCA GGACAGAACC ACAGGCACAC   1877
ACTGAGGGGG CAGTGTGGCT CCCTGCCTGT CCCATCCCCA TGCCCCGTCC GCGGGGCTGT   1937
GGCTGCTGCT GTGCATGTCC CTGCGATGGG AGTCTTGTCT CCCAGCCTGT CAGTTTCCTC   1997
CCCAGGGCAG AGCTCCCCTT CCTGCAAGAG TCTGGGAGGC GGTGCAGGCT GTCCTGGCTG   2057
CTCTGGGGAA GCCGAGGGAC AGCCATAACA CCCCCGGGAC AGTAGGTCTG GGCGGCACCA   2117
CTGGGAACTC TGGACTTGAG TGTGTTTGCT CTTCCTTGGG TATGAATGTG TGAGTTCACC   2177
CAGAGGCCTG CTCTCCTCAC ACATTGTGTG GTTTGGGGTT AATGATGGAG GGAGACACCT   2237
CTTCATAGAC GGCAGGTGCC CACCTTTCAG GGAGTCTCCC AGCATGGGCG GATGCCGGGC   2297
ATGAGCTGCT GTAAACTATT TGTGGCTGTG CTGCTTGAGT GACGTCTCTG TCGTGTGGGT   2357
GCCAAGTGCT TGTGTAGAAA CTGTGTTCTG AGCCCCCTTT TCTGGACACC AACTGTGTCC   2417
TGTGAATGTA TCGCTACTGT GAGCTGTTCC CGCCTAGCCA GGGCCATGTC TTAGGTGCAG   2477
CTGTGCCACG GGTCAGCTGA GCCACAGTCC CAGAACCAAG CTCTCGGTGT CTCGGGCCAC   2537
CATCCGCCCA CCTCGGGCTG ACCCCACCTC CTCCATGGAC AGTGTGAGCC CCGGGCCGTG   2597
CATCCTGCTC AGTGTGGCGT CAGTGTCGGG GCTGAGCCCC TTGAGCTGCT TCAGTGAATG   2657
TACAGTGCCC GGCACGAGCT GAACCTCATG TGTTCCACTC CCAATAAAAG GTTGACAGGG   2717
GCTTCTCCTT CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAA                   2762
```

FIG. 4 (cont'd)

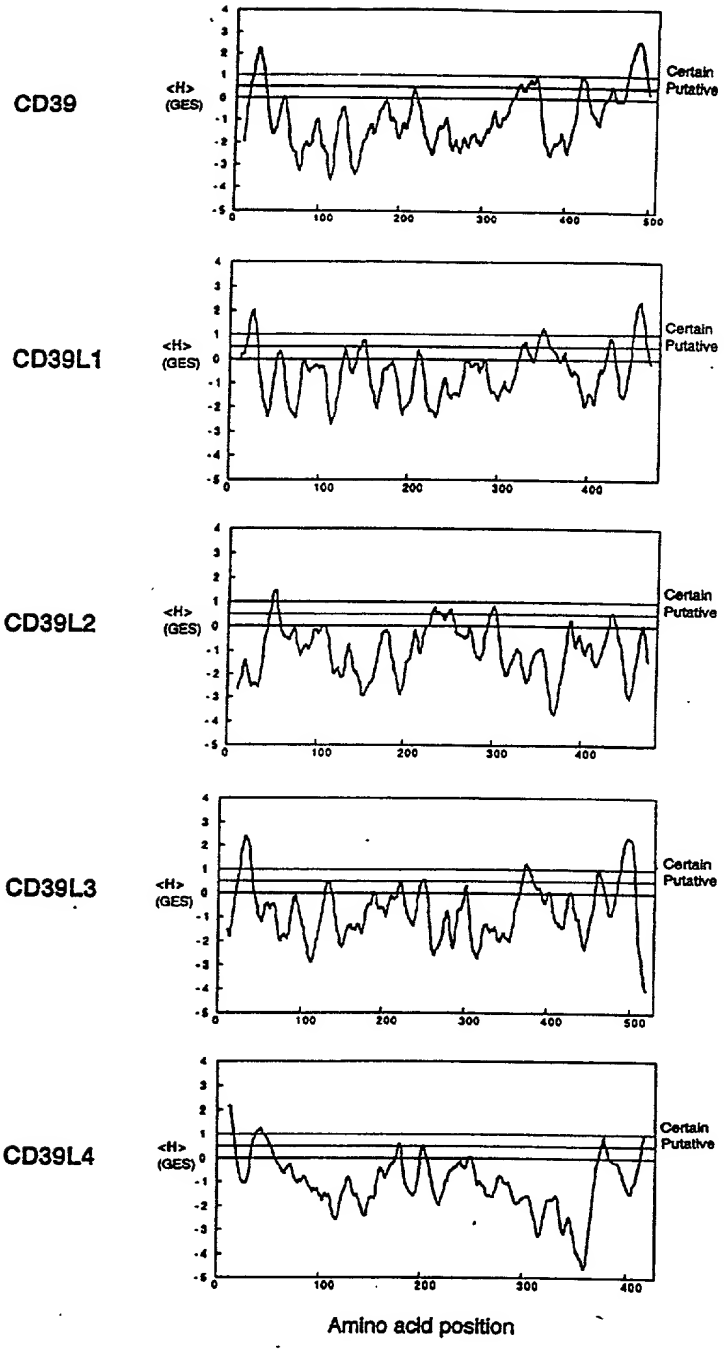
CD39
CD39L1
CD39L2
CD39L3
CD39L4
<H>
(GES)
Certain
Putative
Amino acid position

FIG. 5

```
ACCCACGCGT CTGGCCGCGG GCCGCCTCTG CGGCAGCGCT AGTCGCCTTC TCCGAATCGG      60
 CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT      112
                          Met Phe Thr Val Leu Thr Arg Gln Pro Cys
                           1               5                  10

GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC      160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
                  15                  20                  25

TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC      208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
             30                  35                  40

ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT      256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
         45                  50                  55

ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA      304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
     60                  65                  70

TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC      352
Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
75                   80                  85                  90

AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC      400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
                  95                 100                 105

CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG      448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
             110                 115                 120

CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC      496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
         125                 130                 135

ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT      544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
     140                 145                 150

GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC      592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
155                  160                 165                 170

TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA      640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly
                 175                 180                 185

TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG      688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu
             190                 195                 200

TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG      736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu
         205                 210                 215

GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG      784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys
     220                 225                 230
```

FIG. 6

```
ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC      832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr
235                 240                 245                 250

GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG      880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu
                255                 260                 265

GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA      928
Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys
            270                 275                 280

AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC      976
Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe
        285                 290                 295

ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA     1024
Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro
    300                 305                 310

GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC     1072
Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp
315                 320                 325                 330

CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT     1120
Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala
                335                 340                 345

TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG     1168
Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys
            350                 355                 360

ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT     1216
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser
        365                 370                 375

GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC     1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser
    380                 385                 390

ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC     1312
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu
395                 400                 405                 410

CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC     1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn
                415                 420                 425

TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT     1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr
            430                 435                 440

TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC     1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala
        445                 450                 455

TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA     1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu
    460                 465                 470

AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC     1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr
475                 480                 485                 490
```

FIG. 6 (cont.d.)

```
CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA    1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala
                495                 500                 505

TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT    1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe
            510                 515                 520

GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA TGGC  1703
Asp His Ala Val Asp Ser Asp
        525

TGCTTAGAGT CAGCCTGGGT GGCACCAGGC AATGCAGGTG AAGTGGCTGC CTTCAGGAAA   1763
TACAACTAAC TAAAATCAAA CACCTAGGTC ACGTGCCTCT CAAATACTGA TTTCTGCCAC   1823
AGCACCTCTT GAGGCATCCC TTGGCTATTC TGTGCATATT GTTCTTCAGA GACCTCACTA   1883
CCCACATGCT GATCTATTGG GGAACAGAGA AGAGACAGGC CACTAAGGTC AGGCTCTTTA   1943
TATTAAGTTC CCCAGAGGAA GAGTAAGTTG AGAAGGTATC AGTTTAATGT TGAAGAATTG   2003
ACCTCAGGGC TCAGTTTCCA TTTCCCTCCC TCAGTATTCT TCCTGGCAAG ATACCCATTA   2063
AGCATTTCGC CAATCAGAAT CTCATTTTAT AGTTTTTCCC ATTGGTCTTT AACTAAGACT   2123
TTCTTGTAGC AATCTCGTAA GCAGTGAACC CCCTCAGATC AGTAGAATAT AGTATCTGGG   2183
GGAGAAGACT TACTTCCTTC AGGGCAGCAG CCACAGCCAG GCTTCTGTCA TACAGGTAGA   2243
TCCCGAAGCA CAGAGACATA AAAAAGGTCT CCCAGAAAAC TATAGACCAT TCTCCAAGTG   2303
GAATTCCCAC TTAGGGCTCT GGTCACTAGA TTGCAACCTG TGTGTTTGTC ATCATCCTCA   2363
TCTCACCATT GTATTGCTAT GCCCTCCCAT AAAAACACAT TGATCCCTAG CAAGATTATT   2423
GCATTCCAGA TTTTACTGCC TTTGCTAGGC TTTTGCTTAG CAAAGGGCTG ACTTTCCATT   2483
GTTATCATGG TGTATATATT TTTGTCACCA TTCCCACAAG TATACTTGAT GTTGTCATAG   2543
AACGAACATC CTACTCTATG ATTTACTAAC CAATTACTTT CCCAGATCAT AGACCTCTCT   2603
GCATAGTAGT CATAGGTCTT GACTTTGGGG AAAGAAAAGG AAGCTGCAGG AATATTTATC   2663
TCCAAAGTCG AATGAGAAAG AACTCCAGCA AATCCAATGG CTACAAACTA AAAATCAGCA   2723
TTATTTCATA TTGCTGTTTC TTAGCTGAAT ATGGAATAAA GAACTATTAT TTTATTTTGA   2783
AAAAAAAAAA AAAA                                                     2797
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FIG. 6 (cont'd)

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GCGCGCGCGT TTTCCTTGTT CCTGGTCAAC AAAGAAATGT GGAGTGTCTT GGCTGAATCC     60
TCATACAGAC AAGATCATTA TGGTGCTGTT AGGTAGGACT TGTATCCAGA TGTAAGGTTG    120
AAAAAGTGAT ATAATAAAGG AACCAAGGAG AAAATTCAGA AGGAAAGAAA AAATTGCCTC    180
TGCAGGTGTG CGAGCAGGAT TGCTTCTGCA ACAAAAGCCT CCACCCAGCC ACATCTTGGG    240
AAAAGA ATG GCC ACT TCT TGG GGC ACA GTC TTT TTC ATG CTG GTG GTA        288
       Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val
        1               5                  10

TCC TGT GTT TGC AGC GCT GTC TCC CAC AGG AAC CAG CAG ACT TGG TTT      336
Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe
15                  20                  25                  30

GAG GGT ATC TTC CTG TCT TCC ATG TGC CCC ATC AAT GTC AGC GCC AGC      384
Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser
                35                  40                  45

ACC TTG TAT GGA ATT ATG TTT GAT GCA GGG AGC ACT GGA ACT CGA ATT      432
Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile
            50                  55                  60

CAT GTT TAC ACC TTT GTG CAG AAA ATG CCA GGA CAG CTT CCA ATT CTA      480
His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu
        65                  70                  75

GAA GGG GAA GTT TTT GAT TCT GTG AAG CCA GGA CTT TCT GCT TTT GTA      528
Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val
    80                  85                  90

GAT CAA CCT AAG CAG GGT GCT GAG ACC GTT CAA GGG CTC TTA GAG GTG      576
Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val
95                  100                 105                 110

GCC AAA GAC TCA ATC CCC CGA AGT CAC TGG AAA AAG ACC CCA GTG GTC      624
Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val
                115                 120                 125

CTA AAG GCA ACA GCA GGA CTA CGC TTA CTG CCA GAA CAC AAA GCC AAG      672
Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys
            130                 135                 140

GCT CTG CTC TTT GAG GTA AAG GAG ATC TTC AGG AAG TCA CCT TTC CTG      720
Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu
        145                 150                 155

GTA CCA AAG GGC AGT GTT AGC ATC ATG GAT GGA TCC GAC GAA GGC ATA      768
Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile
    160                 165                 170

TTA GCT TGG GTT ACT GTG AAT TTT CTG ACA GGT CAG CTG CAT GGC CAC      816
Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His
175                 180                 185                 190

AGA CAG GAG ACT GTG GGG ACC TTG GAC CTA GGG GGA GCC TCC ACC CAA      864
Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln
                195                 200                 205

ATC ACG TTC CTG CCC CAG TTT GAG AAA ACT CTG GAA CAA ACT CCT AGG      912
Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg
            210                 215                 220

GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT TAT AAG CTC TAT      960
Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr
        225                 230                 235
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FIG. 7

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ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC     1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr
    240                 245                 250

CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT     1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser
255                 260                 265                 270

GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG     1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val
                275                 280                 285

AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC     1152
Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro
            290                 295                 300

TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA     1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro
        305                 310                 315

GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC     1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp
    320                 325                 330

CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA     1296
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu
335                 340                 345                 350

AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG     1344
Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu
                355                 360                 365

GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC     1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr
            370                 375                 380

ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC     1440
Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val
        385                 390                 395

TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG     1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu
    400                 405                 410

GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC  1539
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
415                 420                 425

GTACTTCCTT GGAGACCTGC ATTTGCCAAC ACCTTTTTAA GGGGAGGAGA GAGCACTTAG  1599
TTTCTGAACT AGTCTGGGAC ATCCTGGACT TGAGCCTAGA GATTTAGGTT TAATTAATTT  1659
TACACATCTA ATGTGAACTG CTGCCTAACC ACTCAAGAGT ACACAGCTGG CACCAGAGCA  1719
TCACAGAGAG CCCTGTGAGC CAAAAAGTAT AGTTTTGGAA CTTAACCTTG GAGTGAGAGC  1779
CCAGGGACAG GTCCCTGGAA ACCAAAGAAA AATCGCATTT CAACCCTTTG AGTGCCTCAT  1839
TCCACTGAAT ATTTAAATTT TCCTCTTAAA TGGTAAACTG ACTTATTGCA ATCCCAAGAC  1899
CCATCAATAT CAGTATTTTT TTCCTCCCTA TACAGTGCCC TGCCCACCCT TATCTGCACC  1959
CACCTCCCCT GAAAAAGAGA GAAAAAAAAA AAAAAAAAA                         1998
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FIG. 7 (cont'd.)

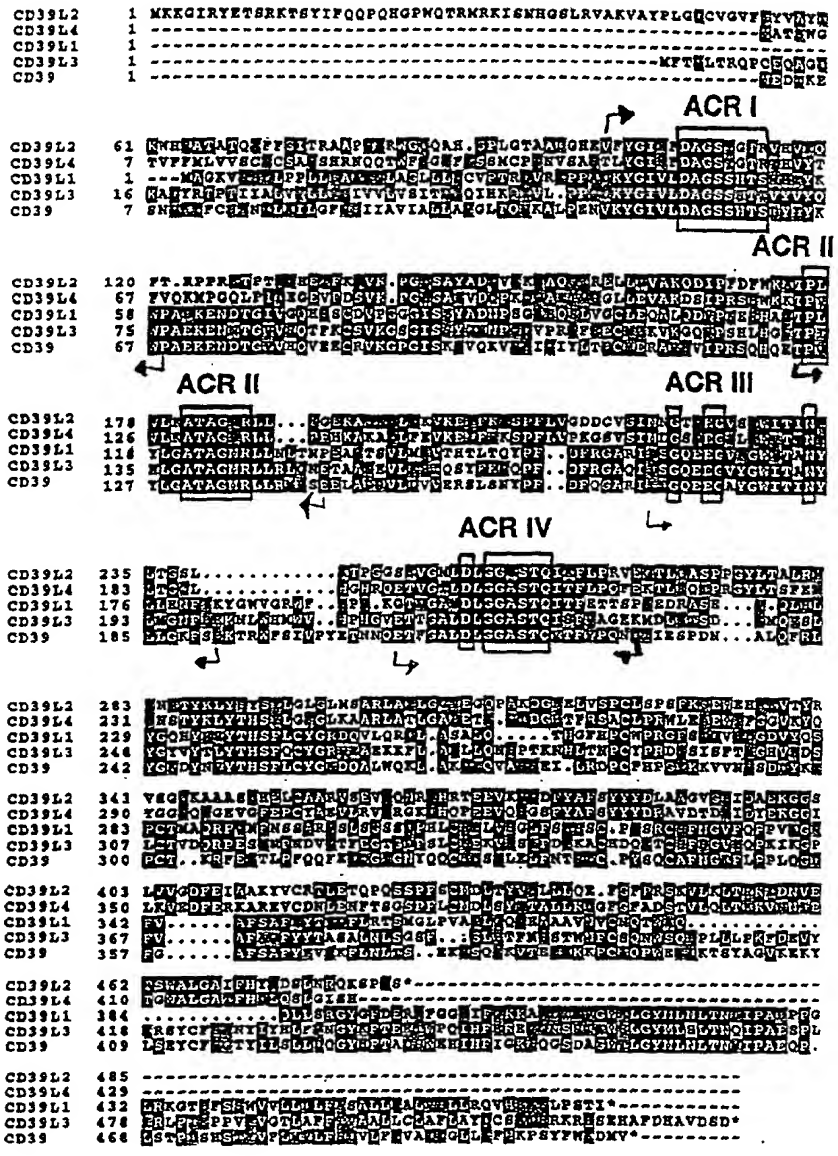

FIG. 8

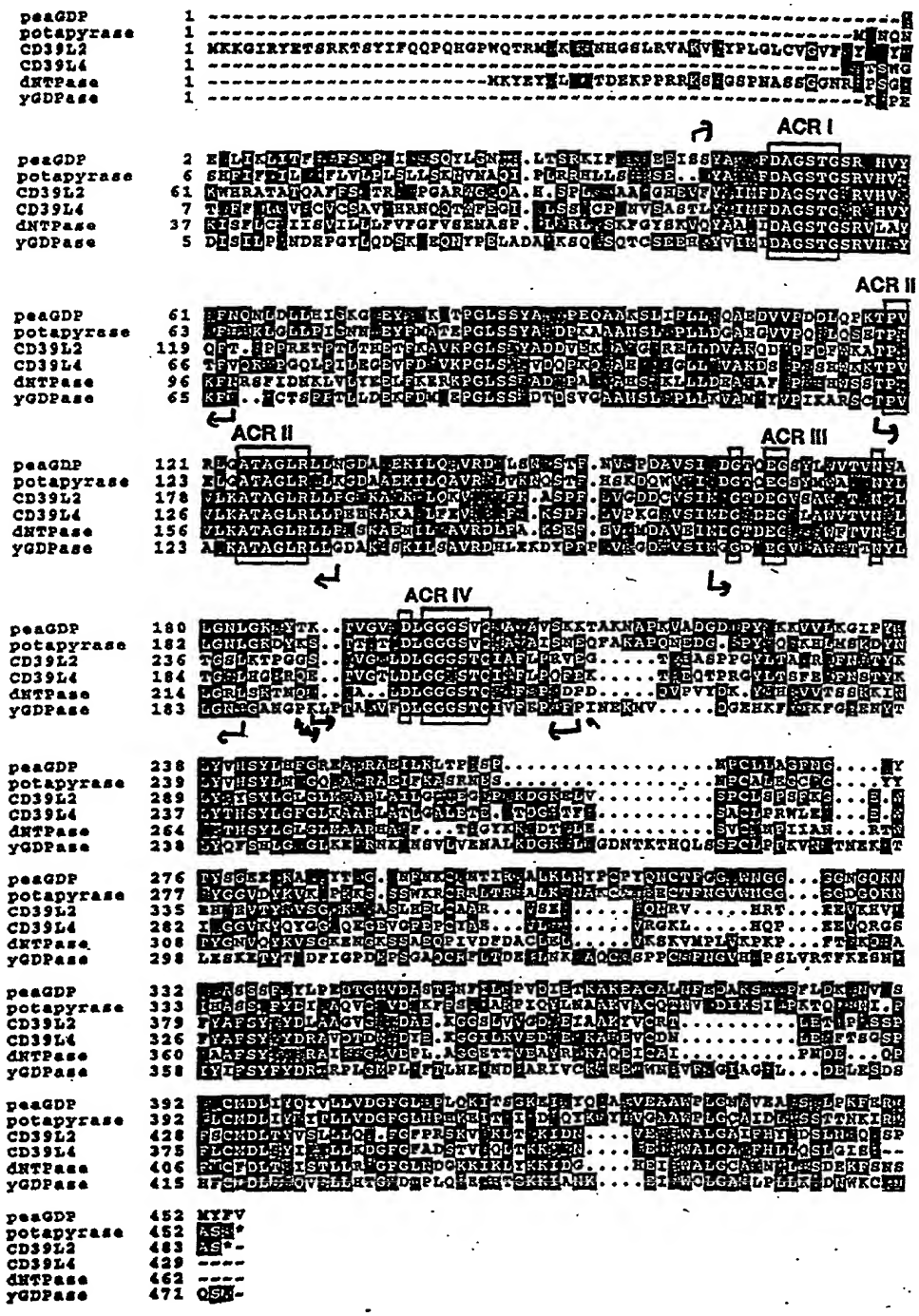

FIG. 9